



PARASITO 2025

29º CONGRESSO BRASILEIRO DE PARASITOLOGIA

INTRA-GENOTYPIC VARIABILITY IN *TRYPANOSOMA CRUZI* DTU TcII

THAINÁ DOS SANTOS DELECRODE^{1,2}, ANA MARIA JANSEN¹, CRISTIANE VARELLA LISBOA¹,
CAROLINA FURTADO³, VALDIRENE DOS SANTOS LIMA³, LUCIANA DE FREITAS CAMPOS
MIRANDA⁴, ALINE FAGUNDES⁴, SAMANTA CRISTINA DAS CHAGAS XAVIER^{1,2}, MARIA
AUGUSTA DARIO^{1,2}

¹LABORATÓRIO DE BIOLOGIA DE TRIPANOSOMATÍDEOS, INSTITUTO OSWALDO CRUZ,
FIOCRUZ, RIO DE JANEIRO, RJ, BRASIL, ²PROGRAMA DE PÓS-GRADUAÇÃO STRICTO
SENSU EM BIOLOGIA COMPUTACIONAL E SISTEMAS, INSTITUTO OSWALDO CRUZ,
FIOCRUZ, RIO DE JANEIRO, RJ, BRASIL, ³LABORATÓRIO DE GENÉTICA, INSTITUTO
NACIONAL DO CÂNCER, RIO DE JANEIRO, RJ, BRASIL, ⁴LABORATÓRIO DE PESQUISA
CLÍNICA E VIGILÂNCIA EM LEISHMANIOSES (INI), FIOCRUZ, RIO DE JANEIRO, RJ, BRASIL.

Abstract

Trypanosoma cruzi is a genetically diverse parasite grouped into seven Discrete Typing Units (DTUs): TcI to TcVI and TcBaT. Due to its association with Chagas disease (CD), studies on TcII in wild animals are rare, and its diversity is poorly understood. This study aimed to analyze TcII variability, testing the hypothesis of genetic variability and that primate and humans select the same sublineages. DNA from TcII isolates (marsupials n=12, primates n=80, humans n=55) were subjected to PCR targeting the 18S rDNA gene, followed by next-generation sequencing on Illumina platform. Sequences were identified by bioinformatics analysis. Genetic distances were analyzed using a matrix (MegaX) and a haplotype network (Network). Four DTU TcII sublineages were identified: alpha, beta, gamma and delta. Alpha was widely distributed and adaptable in all the samples. No genetic distance differences were observed with reference sequences Y, Esmeraldo and Basileu. It was the only sublineage identified in *Didelphis* sp., which may indicate that alpha is the oldest sublineages, because this mammal is considered the ancestor of *T. cruzi*. Beta was found in primate and human, making it the second most widely distributed. Gamma was found only in primates, and delta only in human samples. Gamma was closest genetic distance to alpha (0.002), followed by beta (0.008). Delta was genetically distant from alpha (0.015) and beta (0.023). Human samples showed mixed infections: alpha+beta (n=4) and alpha+delta (n=1). Primate samples showed alpha+beta (n=5) and alpha+gamma (n=1). Beta and gamma sublineages seem to be transmitted by vectors that do not interact with marsupials and delta transmitted by vectors interacting directly with humans. The differentiation between gamma and delta hosts may be due to limited environmental exposure, with gamma being restricted to primates. These findings offer new perspectives on the genetic variability of TcII and its interactions with hosts in nature.

Supported by: CNPq, CAPES, FAPERJ, PG EM BIOLOGIA COMPUTACIONAL E SISTEMAS,
IOC,INI (FIOCRUZ), INCA

Keywords: Intra Genotypic Diversity, *Trypanosoma cruzi* TcII, Primate

 (11) 93232-3976

 www.parasito2025.com

 info@parasito2025.com

60SBP
ANOS
SOCIEDADE BRASILEIRA DE PARASITOLOGIA